

tivities at the end of the Tertiary (PARK 1985). Cheju Island was connected to the Korean peninsula during the Pleistocene and separated again at the end of the last glaciation, about 10000 years ago. Therefore, roe deer in Cheju could have evolved in isolation during the last 10000 years. KOH et al. (1997) reported that roe deer from the Korean peninsula showed smaller body size and skull length than west and east Siberian roe deer subspecies. Thus, molecular and morphological data lend support to the view that roe deer from Korea do not belong neither to *C. p. tianschanicus* nor *C. p. mantschuricus* (= *bedfordi*), and might belong to a distinct subspecies, *C. p. ochracea*, as described by BARCLAY (1935).

Acknowledgements

This research was in part supported by the Korean Science Foundation (grant 97-0402-05-01-3 to HUNG SUN KOH), and by the Italian Istituto Nazionale per la Fauna Selvatica (I.N.F.S.) and Consiglio Nazionale delle Ricerche (C.N.R.).

References

- BARCLAY, E. N. (1935): The roe deer of Korea. *Ann. Mag. Natural History (London)* **15**, 626–627.
- COOK, C. E.; WANG, Y.; SENSABAUGH, G. (1999): A mitochondrial control region and cytochrome *b* phylogeny of sika deer (*Cervus nippon*) and report of tandem repeats in the control region. *Mol. Phylogenet. Evol.* **12** 47–56.
- DANILKIN, A. (1996): Behavioural Ecology of Siberian and European Roe Deer. London: Chapman and Hall.
- DOUZERY, E.; RANDI, E. (1997): The mitochondrial control region of Cervidae: Evolutionary patterns and phylogenetic content. *Mol. Biol. Evol.* **14**, 1154–1166.
- ELLERMAN, J. R.; MORRISON-SCOTT, T. C. S. (1951): Check-list of Palaearctic and Indian Mammals 1758 to 1946. London: British Museum (Natural History).
- FELSENSTEIN, J. (1985): Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**, 783–791.
- GROVES, C. P.; GRUBB, P. (1987): Relationships of living deer. In: *Biology and Management of the Cervidae*. Ed by C. M. WEMMER. Washington (D.C.): Smithsonian Institution Press. Pp. 21–59.
- GRUBB, P. (1993): Order Artiodactyla. In: *Mammal Species of the World: A Taxonomic and Geographic Reference*. Ed. by D. E. WILSON and D. M. REEDER. Washington (D.C.): Smithsonian Institution Press. Pp. 337–414.
- HEPTNER, V. G.; NASIMOVICH, A. A.; BANNIKOV A. G. (1989): *Mammals of the Soviet Union, Ungulates*. Vol. I. Leiden: E. J. Brill.
- HEWISON, A. J. M.; DANILKIN, A. (2001): Evidence for separate specific status of European (*Capreolus capreolus*) and Siberian (*C. pygargus*) roe deer. *Mamm. biol.* **66**, 13–21.
- KOH, H. S.; YOO, S. K.; LEE, B. K.; (1997): Analyses of external and cranial morphology of roe deer (*Capreolus pygargus bedfordi* Thomas) from Korea. *Bull. Nat. Sci. (Chungbuk Univ.)* **11**, 99–103 (in Korean).
- NAGATA, J.; MASUDA, R.; KAJI, K.; KANEKO, M.; YOSHIDA, M. C. (1998): Genetic variation and population structure of the Japanese sika deer (*Cervus nippon*) in Hokkaido Island, based on mitochondrial D-loop sequences. *Mol. Ecol.* **7**, 871–877.
- PARK, D. W. (1985). Geology and coasts and mountains in Cheju Island. *Cheju-Do study (Cheju Province, Korea)* **2**, 321–322.
- RANDI, E.; MUCCI, N.; PIERPAOLI, M.; DOUZERY, E. (1998a): New phylogenetic perspectives on the Cervidae (Artiodactyla) are provided by the mitochondrial cytochrome *b* gene. *Proc. Roy. Soc. Lond., B* **265**, 793–801.
- RANDI, E.; PIERPAOLI, M.; DANILKIN, A. (1998b): Mitochondrial DNA polymorphism in populations of Siberian and European roe deer (*Capreolus pygargus* and *C. capreolus*). *Heredity* **80**, 429–437.
- RANDI, E.; MUCCI, N.; CLARO-HERGUETA, F.; BONNET, A.; DOUZERY, E. J. P. (2001): A mitochondrial DNA control region phylogeny of the Cervinae: Speciation in *Cervus* and implications for conservation. *Animal Conserv.* **4**, 1–11.
- SAITOU, N.; NEI, M. (1987): The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **4**, 406–425.
- SOKOLOV, V. E.; GROMOV, V. S. (1990): The contemporary ideas on roe deer (*Capreolus* Gray, 1821) systematization: Morphological, ethological and hybridological analysis. *Mammalia* **54**, 431–444.
- SWOFFORD, D. L. (1998): PAUP*: Phylogenetic analysis using parsimony (and other meth-

- ods), version 4.0b2a. Sunderland, Massachusetts: Sinauer Associated.
- TAMURA, K.; NET, M. (1993): Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol. Biol. Evol.* **10**, 512–526.
- TATE, G. H. H. (1947): *Mammals of Eastern Asia*. New York: MacMillan Co.
- THOMPSON, J. D.; GIBSON, T. J.; PLEWNIAK, F.; JEANMOUGIN, F.; HIGGINS, D. G. (1997): The CLUSTALX windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucl. Acids. Res.* **24**, 4876–4882.
- Authors' addresses:**
HUNG SUN KOH, Department of Biology, Chungbuk University, Cheongju 361–763, Korea (e-mail: syskoss@cbucc.chungbuk.ac.kr)
ETTORE RANDI, Istituto Nazionale per la Fauna Selvatica, Via Cà Fornacetta, 9, 40064 Ozzano dell'Emilia (BO), Italy



Short communication

A new karyotype of *Heliophobius argenteocinereus* (Bathyergidae, Rodentia) from Zambia with field notes on the species

Von A. SCHARFF, M. MACHOLAN, J. ZIMA and H. BURDA

Department of General Zoology, University of Essen, Essen, Germany; Institute of Vertebrate Biology and Institute of Animal Physiology and Genetics, Academy of Sciences, Brno, Czech Republic

Receipt of Ms. 05. 03. 2001

Acceptance of Ms. 11. 04. 2001

Key words: *Heliophobius argenteocinereus*, Bathyergidae, karyotype, field notes

The silvery mole-rat (*Heliophobius argenteocinereus*) is a little known member of the family Bathyergidae, endemic to east to central Africa eastern of the Great Rift Valley, south of Equator, and north of the Zambezi river, i.e., in Kenya, Tanzania, Zambia, Malawi, and Mozambique (BURDA 2001). The only available information on the biology of *Heliophobius* is based on a few studies concerning physiology (McNAB 1966) and burrowing and activity patterns (JARVIS and SALE 1971; JARVIS 1973). GEORGE (1979) described the karyotype of this species from Kenya. Since it resembled the karyotype of *Heterocephalus glaber* (both having $2n = 60$), she concluded that the whole family Bathyergidae is chromosomally rather conservative.

Regarding the fact that recently a large chromosomal variation (ranging from $2n = 40$ to $2n = 78$) has been found in *Cryptomys*, another bathyergid mole-rat (SCHARFF 1998; BURDA 2001), the question arises in as much the karyotype established for a Kenyan population is representative for the whole genus *Heliophobius* which is distributed across at least 15 latitude degrees. To address this question we have examined karyotypes of *H. argenteocinereus* from Zambia, i.e., close to the southern distributional limit.

Three silvery mole-rats (one male, two females), collected in August 1996 in the Lubalashi Area in the Central Province of Zambia ($14^{\circ}40' S$; $29^{\circ}55' E$) about 160 km east of Lusaka, were examined.

Karyotypes were prepared from bone marrow following the splash method according to FORD and HAMERTON (1956). Chromosomes were differentially stained with the C-banding (SUMNER 1972) and G-banding (SEABRIGHT 1971) methods. Characterisation of chromosomes followed the nomenclature of HSU and BENIRSCHKE (1967).

The diploid chromosome number in all the examined individuals of *Heliophobius argenteocinereus* from Zambia was $2n = 62$. The karyotype consisted of 27 pairs of metacentric and submetacentric chromosomes (autosomes) of decreasing size and 3 pairs of small acrocentrics ($Nfa = 114$). The X-chromosome was the second largest metacentric, while the Y-chromosome was dot-like (most probably metacentric).

The karyotype of *Heliophobius argenteocinereus* from Zambia ($2n = 62$; $Nfa = 114$) is very similar to that of silvery mole-rats from Kenya ($2n = 60$; $Nfa = 114$; GEORGE 1979). The difference between both karyotypes (one pair of metacentrics vs. two pairs